Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:19:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524857.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524857.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:19:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,389,703
Mapped reads	1,285,922 / 92.53%
Unmapped reads	103,781 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,853 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	33,385 / 2.4%
Duplication rate	1.73%
Clipped reads	1,289,777 / 92.81%

2.2. ACGT Content

Number/percentage of A's	19,310,844 / 25.58%
Number/percentage of C's	15,130,039 / 20.04%
Number/percentage of T's	23,146,167 / 30.66%
Number/percentage of G's	17,896,562 / 23.71%
Number/percentage of N's	9,700 / 0.01%
GC Percentage	43.75%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2501

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

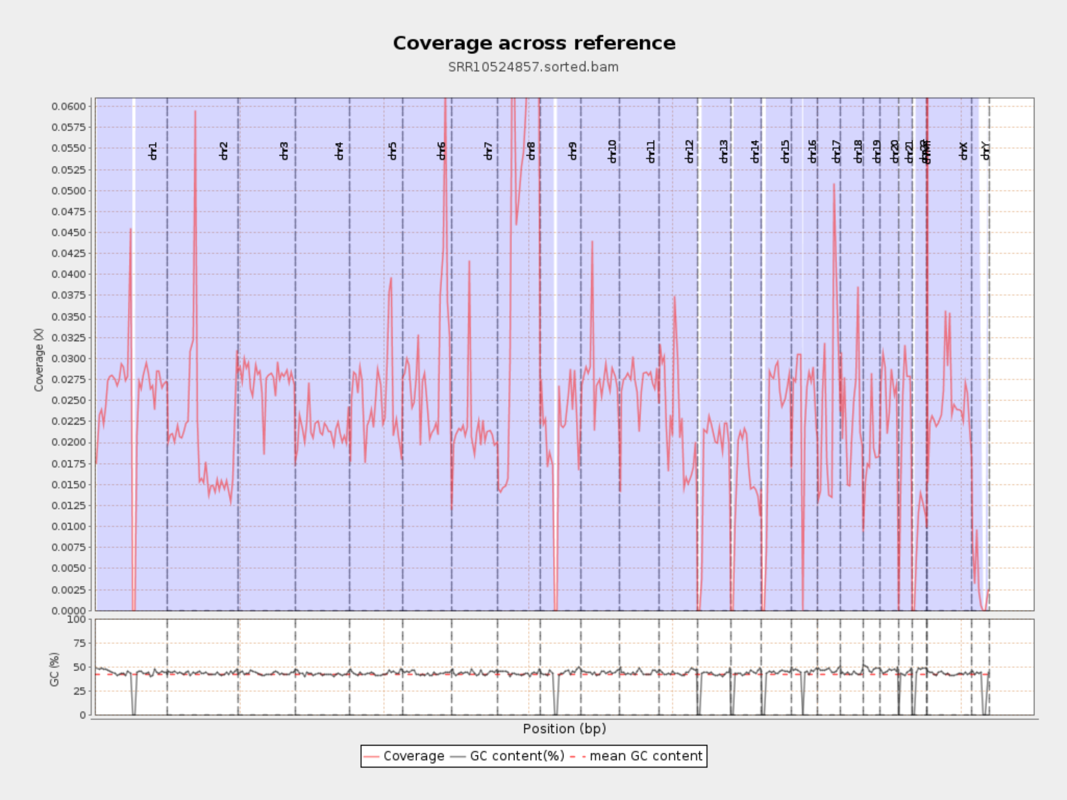
General error rate	0.49%
Mismatches	360,970
Insertions	5,276
Mapped reads with at least one insertion	0.41%
Deletions	14,454
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.55%

2.6. Chromosome stats

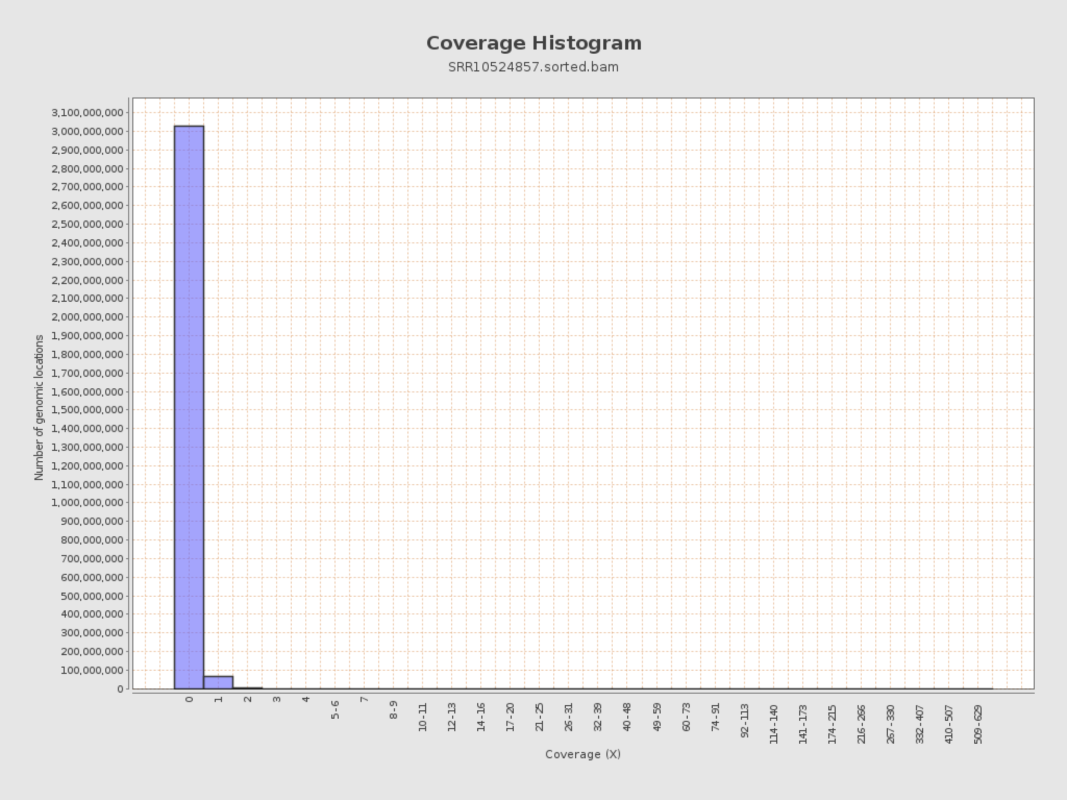
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6316374	0.0253	0.4788
chr2	243199373	4919554	0.0202	0.2458
chr3	198022430	5457457	0.0276	0.1746
chr4	191154276	4107741	0.0215	0.1627
chr5	180915260	4602275	0.0254	0.1693
chr6	171115067	4954341	0.029	0.1964
chr7	159138663	3466090	0.0218	0.3302

chr8	146364022	8159982	0.0558	0.3378
chr9	141213431	2871247	0.0203	0.2033
chr10	135534747	3784358	0.0279	0.2375
chr11	135006516	3642681	0.027	0.2323
chr12	133851895	2991244	0.0223	0.1602
chr13	115169878	2027473	0.0176	0.1412
chr14	107349540	1568220	0.0146	0.1396
chr15	102531392	2240083	0.0218	0.1584
chr16	90354753	2185228	0.0242	0.1777
chr17	81195210	2063080	0.0254	0.1871
chr18	78077248	1838087	0.0235	0.3827
chr19	59128983	1105971	0.0187	0.3365
chr20	63025520	1635331	0.0259	0.1721
chr21	48129895	1092403	0.0227	0.1675
chr22	51304566	456123	0.0089	0.0979
chrMT	16571	8757	0.5285	0.797
chrX	155270560	3840457	0.0247	0.1889
chrY	59373566	181271	0.0031	0.0796

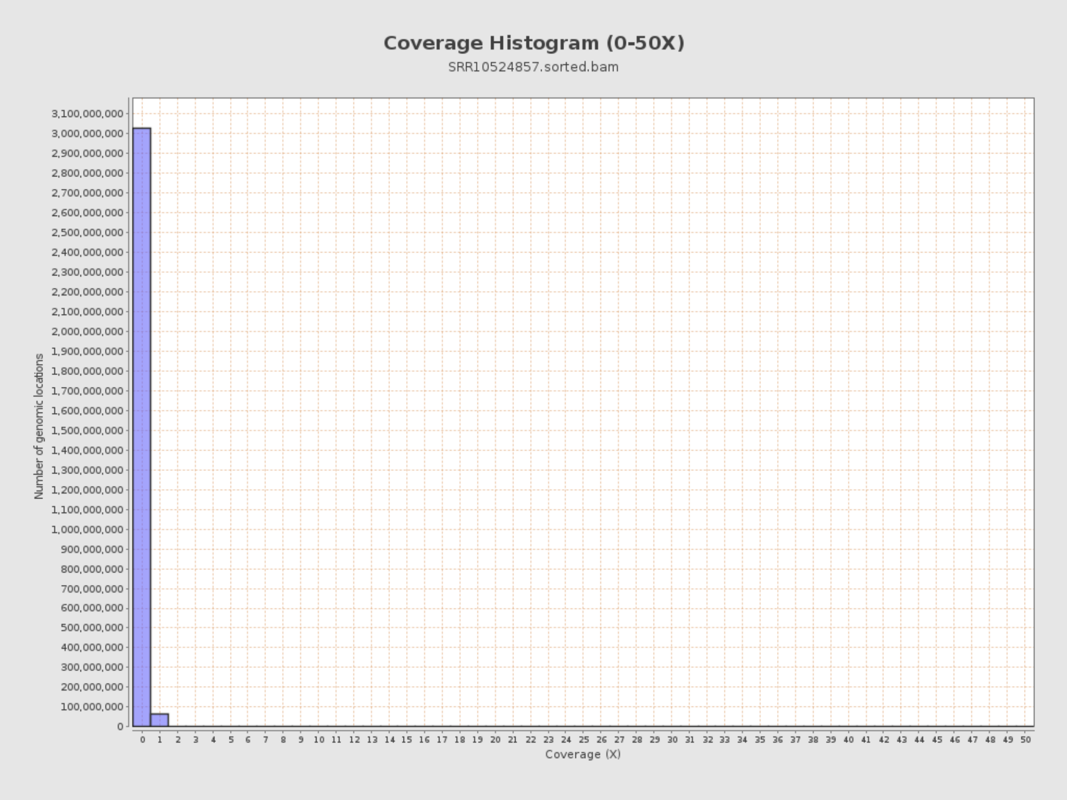
3. Results : Coverage across reference



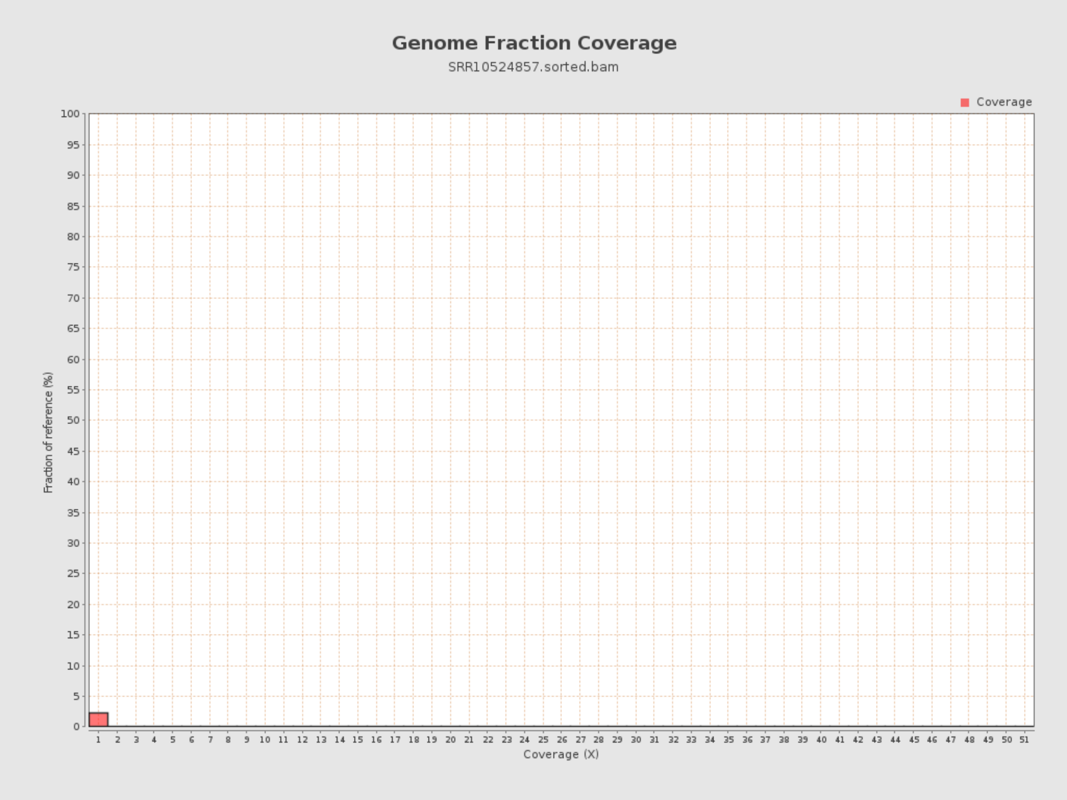
4. Results : Coverage Histogram



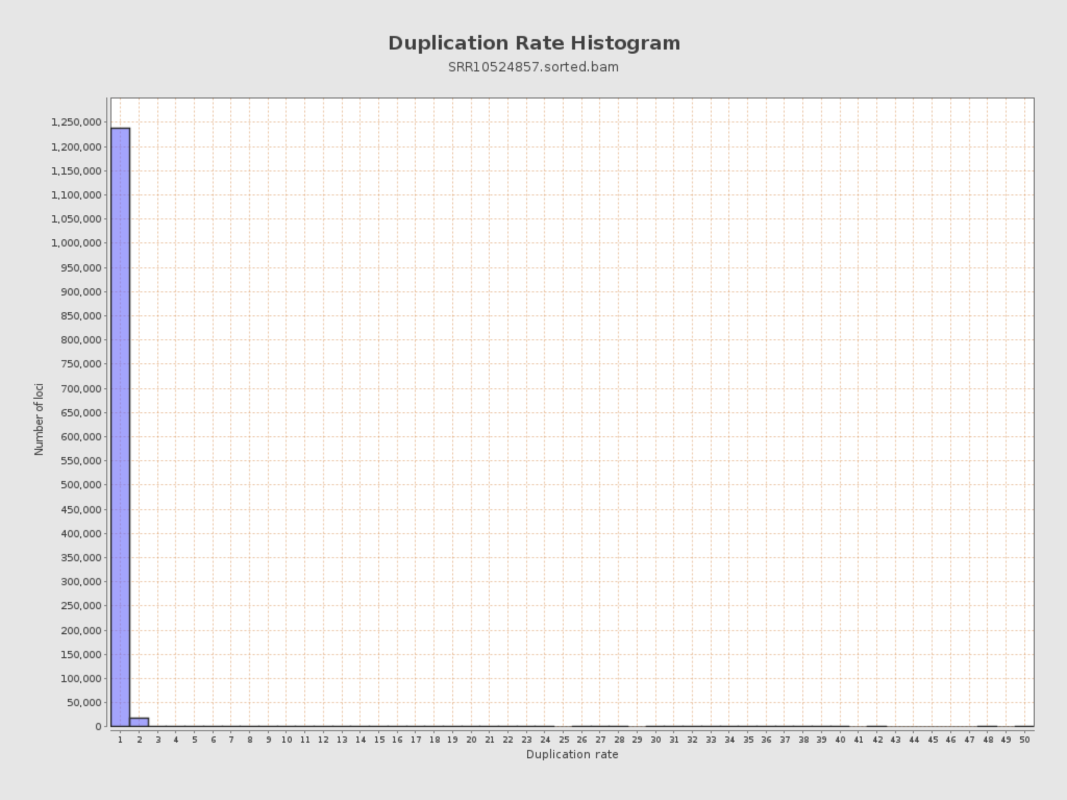
5. Results : Coverage Histogram (0-50X)



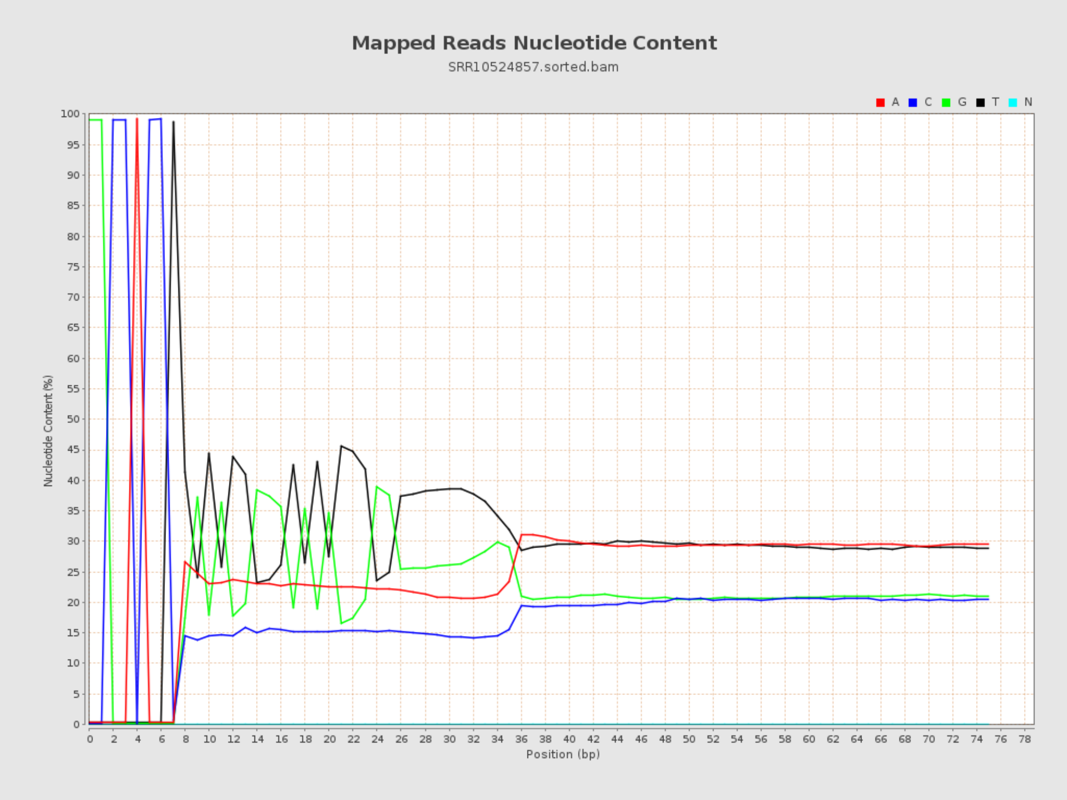
6. Results : Genome Fraction Coverage



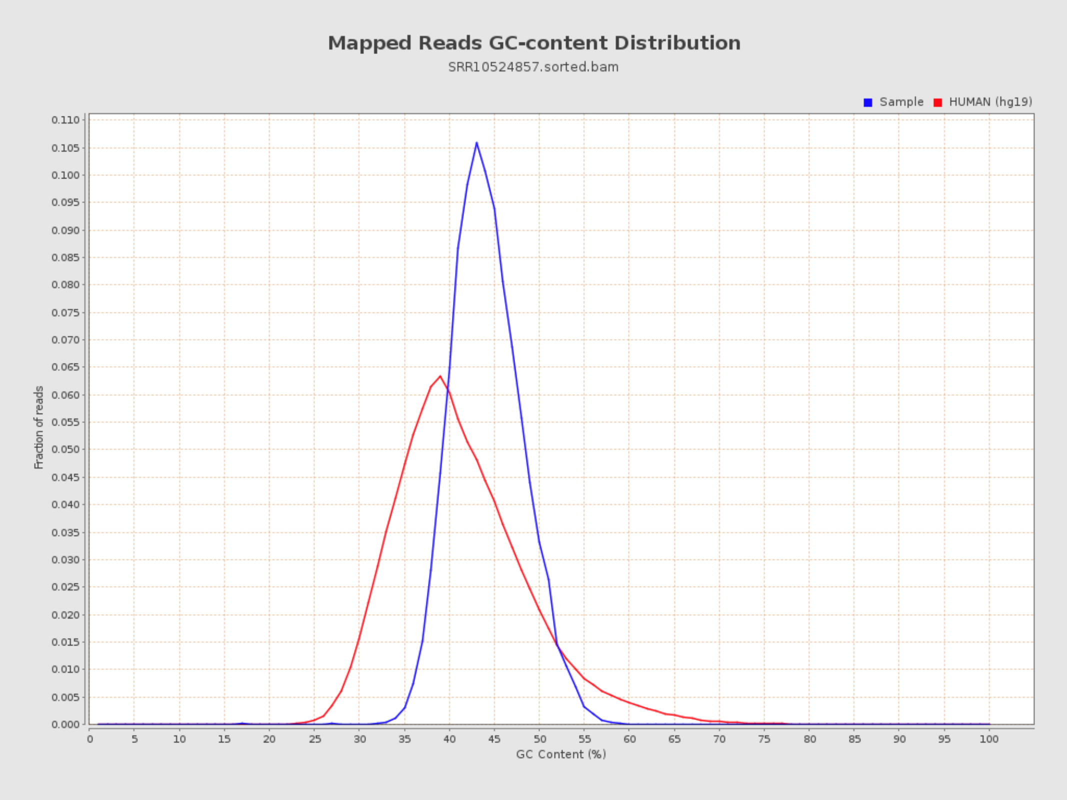
7. Results : Duplication Rate Histogram



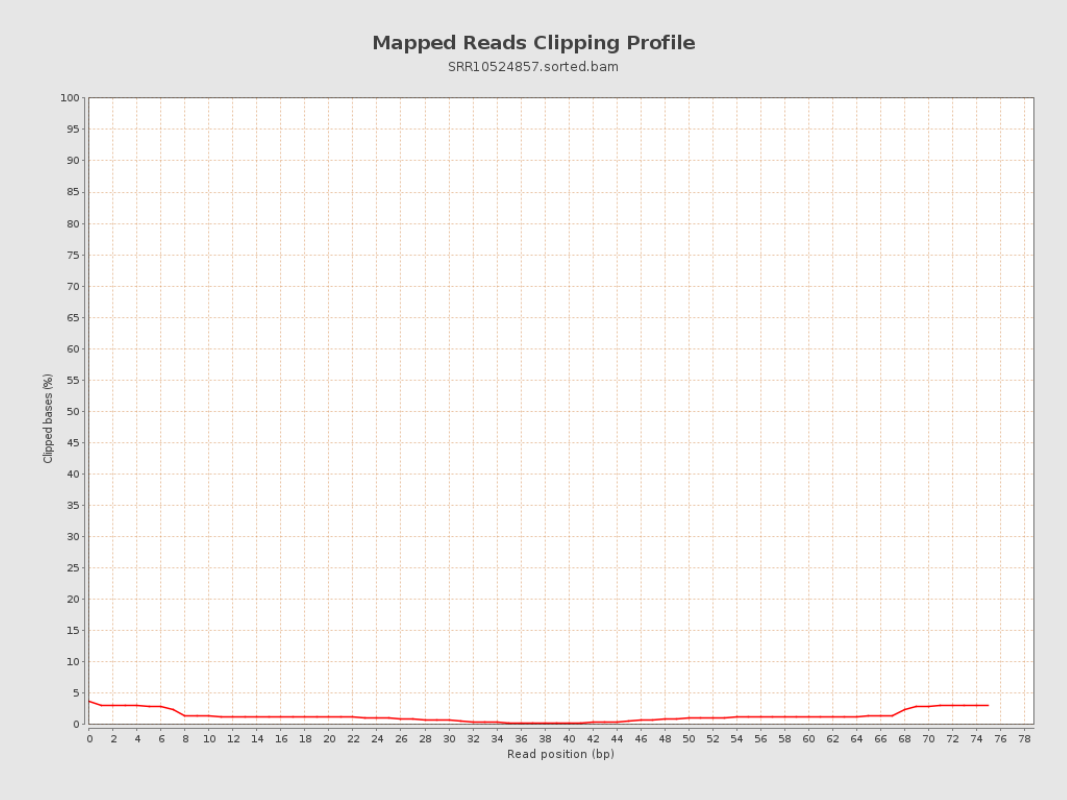
8. Results : Mapped Reads Nucleotide Content



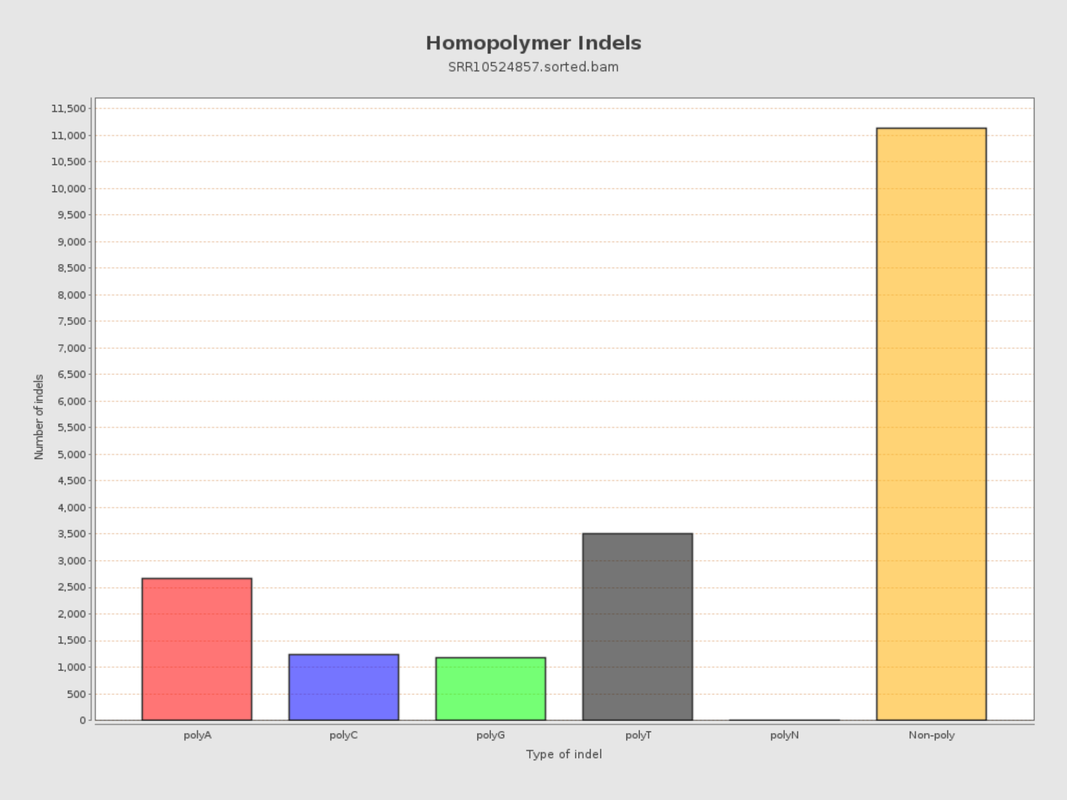
9. Results : Mapped Reads GC-content Distribution



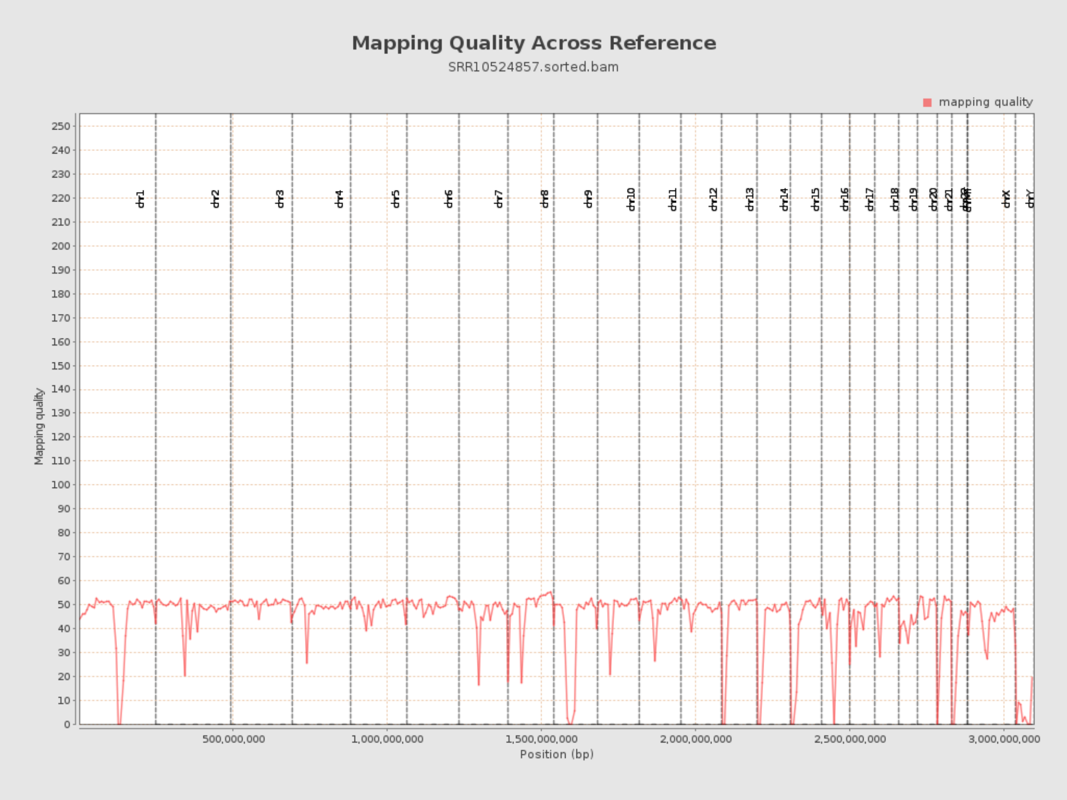
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



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13. Results : Mapping Quality Histogram